

配列表

SEQUENCE LISTING

<110> ASANO Shinichiro et al.

<120> Protein Having Insecticidal Activity, DNA Coding Said Protein, Pest Control Agent and Pest Control Method

<130> BOF-3887PCT

<150> JP 2000-236140

<151> 2000-08-03

<160> 3

<210> 1

<211> 1167

<212> PRT

<213> *Bacillus thuringiensis*

<400> 1

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Leu Asp Ala Ser Ser

1 5 10 15

Ser Thr Ser Val Ser Asp Asn Ser Val Arg Tyr Pro Leu Ala Asn Asp

20 25 30

Gln Thr Thr Thr Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Arg Met

35 40 45

Ser Glu Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile

50 55 60

Ser Ser Ser Thr Val Gln Thr Gly Ile Gly Ile Val Gly Gln Val Leu

65 70 75 80

Gly Ala Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser Phe Tyr Ser

85 90 95

Phe Ile Val Gly Gln Leu Trp Pro Ser Ser Thr Val Ser Val Trp Glu
 100 105 110

Met Ile Met Lys Gln Val Glu Asp Leu Ile Asp Gln Lys Ile Thr Asp
 115 120 125

Ser Val Arg Lys Thr Ala Leu Ala Gly Leu Gln Gly Leu Gly Asp Gly
 130 135 140

Leu Asp Val Tyr Gln Lys Ser Leu Lys Asn Trp Leu Glu Asn Arg Asn
 145 150 155 160

Asp Thr Arg Ala Arg Ser Val Val Val Thr Gln Tyr Ile Ala Leu Glu
 165 170 175

Leu Asp Phe Val Ala Lys Ile Pro Ser Phe Ala Ile Ser Gly Gln Glu
 180 185 190

Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu
 195 200 205

Leu Leu Arg Asp Ala Ser Ile Phe Gly Ala Glu Trp Gly Phe Thr Pro
 210 215 220

Gly Glu Ile Ser Thr Phe Tyr Asp Arg Gln Val Thr Arg Thr Ala Gln
 225 230 235 240

Tyr Ser Asp Tyr Cys Val Lys Trp Tyr Asn Thr Gly Leu Asp Lys Leu
 245 250 255

Lys Gly Thr Asn Ala Ala Ser Trp Leu Lys Tyr His Gln Phe Arg Arg
 260 265 270

Glu Met Thr Leu Leu Val Leu Asp Leu Val Ala Leu Phe Pro Asn Tyr
 275 280 285

Asp Thr Arg Thr Tyr Pro Ile Glu Thr Thr Ala Gln Leu Thr Arg Glu

290	295	300	
Val Tyr Thr Asp Pro Ile Val Phe Asn Arg Glu Thr Ser Gly Gly Phe			
305	310	315	320
Cys Arg Arg Trp Ser Leu Asn Ser Asp Ile Ser Phe Ser Glu Val Glu			
	325	330	335
Ser Ala Val Ile Arg Ser Pro His Leu Phe Asp Ile Leu Ser Glu Ile			
	340	345	350
Glu Phe Tyr Thr Thr Arg Ala Gly Leu Pro Leu Asn Asn Thr Glu Tyr			
	355	360	365
Leu Glu Tyr Trp Val Gly His Ser Ile Lys Tyr Lys Asn Thr Asn Ala			
	370	375	380
Ser Ser Ala Leu Glu Arg Asn Tyr Gly Thr Ile Thr Ser Asn Lys Ile			
385	390	395	400
Lys Tyr Tyr Asp Leu Ala Asn Lys Asp Ile Phe Gln Val Arg Ser Leu			
	405	410	415
Gly Ala Asp Leu Ala Asn Tyr Tyr Ala Gln Val Tyr Gly Val Pro Tyr			
	420	425	430
Ala Ser Phe Thr Leu Leu Asp Lys Asn Thr Gly Ser Gly Ser Val Gly			
	435	440	445
Gly Phe Thr Tyr Ser Lys Pro His Thr Thr Met Gln Val Cys Thr Gln			
	450	455	460
Asn Tyr Asn Thr Ile Asp Glu Ile Pro Pro Glu Asn Glu Pro Leu Ser			
465	470	475	480
Arg Gly Tyr Ser His Arg Leu Ser His Ile Thr Ser Tyr Ser Phe Ser			
	485	490	495

Lys Asn Ala Ser Ser Pro Ala Arg Tyr Gly Asn Leu Pro Val Phe Ala
 500 505 510

Trp Thr His Arg Ser Ala Asp Val Thr Asn Thr Val Tyr Ser Asp Lys
 515 520 525

Ile Thr Gln Ile Pro Val Val Lys Ala His Thr Leu Val Ser Gly Thr
 530 535 540

Thr Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asn Ile Leu Lys Arg
 545 550 555 560

Thr Ser Ser Gly Pro Leu Ala Tyr Thr Ser Val Ser Val Lys Ser Pro
 565 570 575

Leu Ser Gln Arg Tyr Arg Ala Arg Ile Arg Tyr Ala Ser Thr Thr Asn
 580 585 590

Leu Arg Leu Phe Val Thr Ile Ser Gly Thr Arg Ile Tyr Ser Ile Asn
 595 600 605

Val Asn Lys Thr Met Asn Lys Gly Asp Asp Leu Thr Phe Asn Thr Phe
 610 615 620

Asp Leu Ala Thr Ile Gly Thr Ala Phe Thr Phe Ser Asn Tyr Ser Asp
 625 630 635 640

Ser Leu Thr Val Gly Ala Asp Ser Phe Ala Ser Gly Gly Glu Val Tyr
 645 650 655

Val Asp Lys Phe Glu Leu Ile Pro Val Asn Ala Thr Phe Glu Ala Glu
 660 665 670

Glu Asp Leu Asp Val Ala Lys Lys Ala Val Asn Gly Leu Phe Thr Ser
 675 680 685

Lys Lys Asp Ala Leu Gln Thr Ser Val Thr Asp Tyr Gln Val Asn Gln
 690 695 700

Ala Ala Asn Leu Val Glu Cys Leu Ser Asp Glu Leu Tyr Pro Asn Glu
705 710 715 720

Lys Arg Met Leu Trp Asp Ala Val Lys Glu Ala Lys Arg Leu Val Gln
725 730 735

Ala Arg Asn Leu Leu Gln Asp Thr Gly Phe Asn Arg Ile Asn Gly Glu
740 745 750

Asn Gly Trp Thr Gly Ser Thr Gly Ile Glu Val Ala Glu Gly Asp Val
755 760 765

Leu Phe Lys Asp Arg Ser Leu Arg Leu Thr Ser Ala Arg Glu Ile Asp
770 775 780

Thr Glu Thr Tyr Pro Thr Tyr Leu Tyr Gln Gln Ile Asp Glu Ser Leu
785 790 795 800

Leu Lys Pro Tyr Thr Arg Tyr Lys Leu Lys Gly Phe Ile Gly Ser Ser
805 810 815

Gln Asp Leu Glu Ile Lys Leu Ile Arg His Arg Ala Asn Gln Ile Val
820 825 830

Lys Asn Val Pro Asp Asn Leu Leu Pro Asp Val Leu Pro Val Asn Ser
835 840 845

Cys Gly Gly Ile Asp Arg Cys Ser Glu Gln Gln Tyr Val Asp Ala Asn
850 855 860

Leu Ala Leu Glu Asn Asn Gly Glu Asn Gly Asn Met Ser Ser Asp Ser
865 870 875 880

His Ala Phe Ser Phe His Ile Asp Thr Gly Glu Ile Asp Leu Asn Glu
885 890 895

Asn Thr Gly Ile Trp Val Val Phe Lys Ile Pro Thr Thr Asn Gly Tyr

900	905	910
Ala Thr Leu Gly Asn Leu Glu Leu Val Glu Glu Gly Pro Leu Ser Gly		
915	920	925
Glu Thr Leu Glu Arg Ala Gln Gln Gln Glu Gln Gln Trp Gln Asp Lys		
930	935	940
Met Ala Arg Lys Arg Gly Ala Ser Glu Lys Ala Tyr Tyr Ala Ala Lys		
945	950	955
		960
Gln Ala Ile Asp Arg Leu Phe Ala Asp Tyr Gln Asp Gln Lys Leu Asn		
	965	970
		975
Ser Gly Val Glu Met Ser Asp Met Leu Ala Ala Gln Asn Leu Val Gln		
	980	985
		990
Ser Ile Pro Tyr Val Tyr Asn Asp Ala Leu Pro Glu Ile Pro Gly Met		
	995	1000
		1005
Asn Tyr Thr Ser Phe Thr Glu Leu Thr Asn Arg Leu Gln Gln Ala Trp		
	1010	1015
		1020
Asn Leu Tyr Asp Leu Arg Asn Ala Ile Pro Asn Gly Asp Phe Arg Asn		
	1025	1030
		1035
		1040
Gly Leu Ser Asp Trp Asn Ala Thr Ser Asp Val Asn Val Gln Gln Leu		
	1045	1050
		1055
Ser Asp Thr Ser Val Leu Val Ile Pro Asn Trp Asn Ser Gln Val Ser		
	1060	1065
		1070
Gln Gln Phe Thr Val Gln Pro Asn Tyr Arg Tyr Val Leu Arg Val Thr		
	1075	1080
		1085
Ala Arg Lys Glu Gly Val Gly Asp Gly Tyr Val Ile Ile Arg Asp Gly		
	1090	1095
		1100

Ala Asn Gln Thr Glu Thr Leu Thr Phe Asn Ile Cys Asp Asp Asp Thr
 1105 1110 1115 1120

Gly Val Leu Ser Ala Asp Gln Thr Ser Tyr Ile Thr Lys Thr Val Glu
 1125 1130 1135

Phe Thr Pro Ser Thr Glu Gln Val Trp Ile Asp Met Ser Glu Thr Glu
 1140 1145 1150

Gly Val Phe Asn Ile Glu Ser Val Glu Leu Val Leu Glu Glu Glu
 1155 1160 1165

<210> 2

<211> 3504

<212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (1).. (3501)

<400> 2

atg agt cca aat aat caa aat gaa tat gaa att cta gat gct tca tca 48
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Leu Asp Ala Ser Ser
 1 5 10 15

tct act tct gta tcc gat aat tct gtt aga tac cct tta gca aac gat 96
 Ser Thr Ser Val Ser Asp Asn Ser Val Arg Tyr Pro Leu Ala Asn Asp
 20 25 30

caa acg acc aca tta caa aac atg aac tat aaa gat tat ctg aga atg 144
 Gln Thr Thr Thr Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Arg Met
 35 40 45

tct gag gga gag aat cct gaa tta ttt gga aat ccg gag acg ttt att 192

Ser Glu Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile
 50 55 60

agt tca tct acg gtt caa act gga att ggc att gtt ggt caa gta ctg 240
 Ser Ser Ser Thr Val Gln Thr Gly Ile Gly Ile Val Gly Gln Val Leu
 65 70 75 80

ggg gct tta ggg gtt cca ttt gct gga cag ata gct agt ttt tat agt 288
 Gly Ala Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser Phe Tyr Ser
 85 90 95

ttc att gtc ggt caa tta tgg cca tca agt acc gtg agt gta tgg gaa 336
 Phe Ile Val Gly Gln Leu Trp Pro Ser Ser Thr Val Ser Val Trp Glu
 100 105 110

atg att atg aaa caa gtg gaa gat cta att gat caa aaa ala aca gat 384
 Met Ile Met Lys Gln Val Glu Asp Leu Ile Asp Gln Lys Ile Thr Asp
 115 120 125

tct gta agg aaa aca gcg ctt gca gga cta caa gga tta gga gat ggc 432
 Ser Val Arg Lys Thr Ala Leu Ala Gly Leu Gln Gly Leu Gly Asp Gly
 130 135 140

tta gac gta tat cag aaa tca ctt aag aat tgg ctg gaa aat cgt aat 480
 Leu Asp Val Tyr Gln Lys Ser Leu Lys Asn Trp Leu Glu Asn Arg Asn
 145 150 155 160

gat aca aga gct aga agt gtt gtg gtg acc caa tat ata gct tta gag 528
 Asp Thr Arg Ala Arg Ser Val Val Val Thr Gln Tyr Ile Ala Leu Glu
 165 170 175

ctt gat ttt gtt gct aaa atc cca tct ttt gca ata tct gga cag gaa 576
 Leu Asp Phe Val Ala Lys Ile Pro Ser Phe Ala Ile Ser Gly Gln Glu
 180 185 190

gta cca tta tta tca gig tat gca caa gca gcg aat tta cat ttg cta 624
 Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu
 195 200 205

tta tta cga gat gct tcc att ttt gga gca gag tgg gga ttc aca cca 672
 Leu Leu Arg Asp Ala Ser Ile Phe Gly Ala Glu Trp Gly Phe Thr Pro
 210 215 220

gga gaa att tcc aca ttt tat gat cgt cag gtg aca cgt acc gcc caa 720
 Gly Glu Ile Ser Thr Phe Tyr Asp Arg Gln Val Thr Arg Thr Ala Gln
 225 230 235 240

tac tcg gat tat tgt gta aag tgg tat aac act ggc tta gat aaa tta 768
 Tyr Ser Asp Tyr Cys Val Lys Trp Tyr Asn Thr Gly Leu Asp Lys Leu
 245 250 255

aaa ggt acg aat gct gca agt tgg ctg aag tat cac caa ttc cga aga 816
 Lys Gly Thr Asn Ala Ala Ser Trp Leu Lys Tyr His Gln Phe Arg Arg
 260 265 270

gaa atg aca tta ctg gta tta gat tta gta gcg tta ttt cca aac tat 864
 Glu Met Thr Leu Leu Val Leu Asp Leu Val Ala Leu Phe Pro Asn Tyr
 275 280 285

gac aca cgt acg tat cca atc gaa aca acg gcc caa ctt aca cgg gaa 912
 Asp Thr Arg Thr Tyr Pro Ile Glu Thr Thr Ala Gln Leu Thr Arg Glu
 290 295 300

gtg tat aca gat cca ata gta ttt aac aga gaa aca agt ggt gga ttt 960
 Val Tyr Thr Asp Pro Ile Val Phe Asn Arg Glu Thr Ser Gly Gly Phe
 305 310 315 320

tgt agg cgt tgg tca ctt aac agt gat att tct ttt tca gaa gtc gaa 1008
 Cys Arg Arg Trp Ser Leu Asn Ser Asp Ile Ser Phe Ser Glu Val Glu
 325 330 335

agc gct gta att cgt tca cca cac cta ttt gat ata ctc agt gaa ata 1056
 Ser Ala Val Ile Arg Ser Pro His Leu Phe Asp Ile Leu Ser Glu Ile
 340 345 350

gaa ttt tat aca aca aga gcg ggg ctt ccc ttg aat aat acg gaa tac 1104

Glu Phe Tyr Thr Thr Arg Ala Gly Leu Pro Leu Asn Asn Thr Glu Tyr	
355	360 365
cct gaa tat tgg gta gga cat tct ata aaa tat aaa aat acg aat gcc 1152	
Leu Glu Tyr Trp Val Gly His Ser Ile Lys Tyr Lys Asn Thr Asn Ala	
370	375 380
tca tca gca tta gaa cgt aat tac ggt acg att act tct aac aaa atc 1200	
Ser Ser Ala Leu Glu Arg Asn Tyr Gly Thr Ile Thr Ser Asn Lys Ile	
385	390 395 400
aag tat tat gat tta gca aat aag gat atc ttt cag gtt cga tca tta 1248	
Lys Tyr Tyr Asp Leu Ala Asn Lys Asp Ile Phe Gln Val Arg Ser Leu	
405	410 415
ggg gcg gat tta gct aat tac tac gca cag gta tat gga gtt ccg tac 1296	
Gly Ala Asp Leu Ala Asn Tyr Tyr Ala Gln Val Tyr Gly Val Pro Tyr	
420	425 430
gct agt ttt aca ctg ctt gac aag aat aca gga tca gga tca gtt gga 1344	
Ala Ser Phe Thr Leu Leu Asp Lys Asn Thr Gly Ser Gly Ser Val Gly	
435	440 445
ggt ttt acg tac tca aaa cca cat aca act atg caa gta tgt aca caa 1392	
Gly Phe Thr Tyr Ser Lys Pro His Thr Thr Met Gln Val Cys Thr Gln	
450	455 460
aat tac aat acg att gat gaa atc cct cca gag aat gag cca ctt agt 1440	
Asn Tyr Asn Thr Ile Asp Glu Ile Pro Pro Glu Asn Glu Pro Leu Ser	
465	470 475 480
aga ggg tat agc cat aga tta tct cat atc acc tct tat tct ttt tct 1488	
Arg Gly Tyr Ser His Arg Leu Ser His Ile Thr Ser Tyr Ser Phe Ser	
485	490 495
aag aat gct agt agt cct gct aga tat ggc aat ctc cct gta ttt gct 1536	
Lys Asn Ala Ser Ser Pro Ala Arg Tyr Gly Asn Leu Pro Val Phe Ala	
500	505 510

l g g a c a c a t c g g a g l g c g g a t g t t a c a a a t a c a g t t t a t t c a g a t a a a 1584
 Trp Thr His Arg Ser Ala Asp Val Thr Asn Thr Val Tyr Ser Asp Lys
 515 520 525

a t t a c t c a g a l a c c a g t t g l a a a g g c a c a t a c t t t a g t t t c a g g t a c t 1632
 Ile Thr Gln Ile Pro Val Val Lys Ala His Thr Leu Val Ser Gly Thr
 530 535 540

a c t g t t a t t a a a g g t c c t g g a t t t a c a g g a g g c a a t a t c c t t a a a a g a 1680
 Thr Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asn Ile Leu Lys Arg
 545 550 555 560

a c a a g t a g t g g t c c g t t a g c t t a t a c t a g t g t c t c t g l a a a t c a c c a 1728
 Thr Ser Ser Gly Pro Leu Ala Tyr Thr Ser Val Ser Val Lys Ser Pro
 565 570 575

t t a t c a c a a a g a t a t c g t g c a a g a a t a c g t t a t g c t t c t a c t a c t a a c 1776
 Leu Ser Gln Arg Tyr Arg Ala Arg Ile Arg Tyr Ala Ser Thr Thr Asn
 580 585 590

t t a c g a c t t t t t g l a a c a a t t t c t g g a a c t c g c a t t t a c t c t a t a a t 1824
 Leu Arg Leu Phe Val Thr Ile Ser Gly Thr Arg Ile Tyr Ser Ile Asn
 595 600 605

g t t a a t a a a a c c a t g a a t a a a g g g g a t g a t t t a a c a t t t a a t a c a t t t 1872
 Val Asn Lys Thr Met Asn Lys Gly Asp Asp Leu Thr Phe Asn Thr Phe
 610 615 620

g a c t t a g c a a c t a t t g g t a c t g c t t t c a c a t t t t c a a a t t a c t c g g a t 1920
 Asp Leu Ala Thr Ile Gly Thr Ala Phe Thr Phe Ser Asn Tyr Ser Asp
 625 630 635 640

a g c t t a a c g g l a g g t g c a g a t t c t t t t g c t t c a g g a g g a g a a g t t t a t 1968
 Ser Leu Thr Val Gly Ala Asp Ser Phe Ala Ser Gly Gly Glu Val Tyr
 645 650 655

g l a g a t a a g t t c g a a c t t a t t c c g g t a a a t g c a a c a t t t g a a g c a g a a 2016

Val Asp Lys Phe Glu Leu Ile Pro Val Asn Ala Thr Phe Glu Ala Glu
 660 665 670

gaa gac cta gat gig gca aag aaa gca gta aat ggc ttg ttt acg agt 2064
 Glu Asp Leu Asp Val Ala Lys Lys Ala Val Asn Gly Leu Phe Thr Ser
 675 680 685

aaa aaa gat gcc tta cag aca agt gta acg gat tat caa gig aat caa 2112
 Lys Lys Asp Ala Leu Gln Thr Ser Val Thr Asp Tyr Gln Val Asn Gln
 690 695 700

gcg gca aac tta gta gaa tgc cta tcc gat gag tta tac cca aat gaa 2160
 Ala Ala Asn Leu Val Glu Cys Leu Ser Asp Glu Leu Tyr Pro Asn Glu
 705 710 715 720

aaa cga atg tta tgg gat gca gtg aaa gag gcg aaa cga ctt gtt cag 2208
 Lys Arg Met Leu Trp Asp Ala Val Lys Glu Ala Lys Arg Leu Val Gln
 725 730 735

gca cgt aac tta ctc caa gat aca ggc ttt aat agg att aat gga gaa 2256
 Ala Arg Asn Leu Leu Gln Asp Thr Gly Phe Asn Arg Ile Asn Gly Glu
 740 745 750

aac gga tgg acg gga agt acg gga atc gag gtt gcg gaa gga gat gtt 2304
 Asn Gly Trp Thr Gly Ser Thr Gly Ile Glu Val Ala Glu Gly Asp Val
 755 760 765

ctg ttt aaa gat cgt tcg ctt cgt ttg aca agt gcg aga gag att gat 2352
 Leu Phe Lys Asp Arg Ser Leu Arg Leu Thr Ser Ala Arg Glu Ile Asp
 770 775 780

aca gaa aca tat cca acg tat ctc tat caa caa ata gat gaa tca ctt 2400
 Thr Glu Thr Tyr Pro Thr Tyr Leu Tyr Gln Gln Ile Asp Glu Ser Leu
 785 790 795 800

tta aaa cca tat aca aga tat aaa cta aaa ggt ttt ata gga agt agt 2448
 Leu Lys Pro Tyr Thr Arg Tyr Lys Leu Lys Gly Phe Ile Gly Ser Ser
 805 810 815

caa gat tta gag att aaa tta ata cgt cat cgg gca aat caa atc gtc 2496
 Gln Asp Leu Glu Ile Lys Leu Ile Arg His Arg Ala Asn Gln Ile Val
 820 825 830

aaa aat gla cca gat aat ctc ttg cca gat gla ctc cct gtc aat tct 2544
 Lys Asn Val Pro Asp Asn Leu Leu Pro Asp Val Leu Pro Val Asn Ser
 835 840 845

tgt ggt ggg atc gat cgc tgc agt gag caa cag tat gla gac gcg aat 2592
 Cys Gly Gly Ile Asp Arg Cys Ser Glu Gln Gln Tyr Val Asp Ala Asn
 850 855 860

tta gca ctc gaa aac aat gga gaa aat gga aat atg tct tct gat tcc 2640
 Leu Ala Leu Glu Asn Asn Gly Glu Asn Gly Asn Met Ser Ser Asp Ser
 865 870 875 880

cat gca ttt tct ttc cat att gat aca ggt gaa ata gat ttg aat gaa 2688
 His Ala Phe Ser Phe His Ile Asp Thr Gly Glu Ile Asp Leu Asn Glu
 885 890 895

aat aca gga att tgg gtc gta ttt aaa att ccg aca aca aat gga tac 2736
 Asn Thr Gly Ile Trp Val Val Phe Lys Ile Pro Thr Thr Asn Gly Tyr
 900 905 910

gca aca cta gga aat ctt gaa ttg gta gaa gag ggg cca ttg tca ggg 2784
 Ala Thr Leu Gly Asn Leu Glu Leu Val Glu Glu Gly Pro Leu Ser Gly
 915 920 925

gaa aca tta gaa cga gca caa caa caa gaa caa caa tgg caa gac aaa 2832
 Glu Thr Leu Glu Arg Ala Gln Gln Gln Glu Gln Gln Trp Gln Asp Lys
 930 935 940

atg gca aga aaa cgt ggg gca tca gaa aaa gca tat tat gca gca aag 2880
 Met Ala Arg Lys Arg Gly Ala Ser Glu Lys Ala Tyr Tyr Ala Ala Lys
 945 950 955 960

caa gcc att gat cgt tta ttc gca gat tat caa gac caa aaa ctt aat 2928

Gln Ala Ile Asp Arg Leu Phe Ala Asp Tyr Gln Asp Gln Lys Leu Asn
 965 970 975

tct ggt gta gaa atg tca gat atg ttg gca gcc caa aac ctt gta cag 2976
 Ser Gly Val Glu Met Ser Asp Met Leu Ala Ala Gln Asn Leu Val Gln
 980 985 990

tcc att cct tac gta tat aat gat gcg tta cca gaa atc cct gga atg 3024
 Ser Ile Pro Tyr Val Tyr Asn Asp Ala Leu Pro Glu Ile Pro Gly Met
 995 1000 1005

aac tat acg agt ttt aca gag tta aca aat aga ctc caa caa gca tgg 3072
 Asn Tyr Thr Ser Phe Thr Glu Leu Thr Asn Arg Leu Gln Gln Ala Trp
 1010 1015 1020

aat ttg tat gat ctt cga aat gct ata cca aat gga gat ttt cga aat 3120
 Asn Leu Tyr Asp Leu Arg Asn Ala Ile Pro Asn Gly Asp Phe Arg Asn
 1025 1030 1035 1040

gga tta agt gat tgg aat gca aca tca gat gtg aat gtg caa caa cta 3168
 Gly Leu Ser Asp Trp Asn Ala Thr Ser Asp Val Asn Val Gln Gln Leu
 1045 1050 1055

agc gat aca tct gtc ctt gtc att cca aac tgg aat tct caa gtg tca 3216
 Ser Asp Thr Ser Val Leu Val Ile Pro Asn Trp Asn Ser Gln Val Ser
 1060 1065 1070

caa caa ttt aca gtt caa ccg aat tat aga tat gtg tta cgt gtc aca 3264
 Gln Gln Phe Thr Val Gln Pro Asn Tyr Arg Tyr Val Leu Arg Val Thr
 1075 1080 1085

gcg aga aaa gag gga gta gga gac gga tat gtg atc atc cgt gat ggt 3312
 Ala Arg Lys Glu Gly Val Gly Asp Gly Tyr Val Ile Ile Arg Asp Gly
 1090 1095 1100

gcg aat cag aca gaa aca ctc aca ttt aat ata tgt gat gat gat aca 3360
 Ala Asn Gln Thr Glu Thr Leu Thr Phe Asn Ile Cys Asp Asp Asp Thr
 1105 1110 1115 1120

ggt gtt tta tct gct gat caa act agc tat atc aca aaa aca gtg gaa 3408
 Gly Val Leu Ser Ala Asp Gln Thr Ser Tyr Ile Thr Lys Thr Val Glu

1125

1130

1135

ttc act cca tct aca gag caa gtt tgg att gac atg agt gag acc gaa 3456
 Phe Thr Pro Ser Thr Glu Gln Val Trp Ile Asp Met Ser Glu Thr Glu

1140

1145

1150

ggt gla ttc aac ata gaa agt gla gaa ctc gtg tta gaa gaa gag taa 3504
 Gly Val Phe Asn Ile Glu Ser Val Glu Leu Val Leu Glu Glu Glu

1155

1160

1165

<210> 3

<211> 3690

<212> DNA

<213> *Bacillus thuringiensis*

<400> 3

gaattctaat gacacagtag aatatttita aaataaagat ggaagggggg atatgaaaaa 60
 tataatcaca agagtcatac aaaaagatgg ttatgtttaa acaaaaaaat cctgtaggaa 120
 taagggttta aaagcaatcg ttgaaaaga tagttatatt aaattgtatg tataggggga 180
 aaaaagatga gtccaaataa tcaaaatgaa tatgaaattc tagatgcttc atcatctact 240
 tctgtatccg ataattctgt tagataccct ttagcaaacg atcaaacgac cacattacaa 300
 aacatgaact ataaagatta tctgagaatg tctgaggag agaatcctga attatttggg 360
 aatccggaga cgtttattag ttcatctacg gticaaacg gaattggcat tgttgggtcaa 420
 gtactggggg ctttaggggt tccatttgcg ggacagatag ctagtittta tagtttcat 480
 gtccgtcaat tatggccatc aagtaccgtg agtgtatggg aaatgattat gaaacaagt 540
 gaagatctaa ttgatcaaaa aataacagat tctgttaagga aaacagcgct tgcaggacta 600
 caaggattag gagatggctt agacgtatat cagaaatcac ttaagaattg gctggaaaa 660
 cgtaatgata caagagctag aagtgttgig gtgacccaat atatagcttt agagcttgat 720
 ttgtttgcta aaatcccatc ttgtgcaata tctggacagg aagttaccatt attatcagt 780
 tatgcacaag cagcgaattt acatttgcta ttattacgag atgcttccat ttgttgagca 840
 gagtggggat tcacaccagg agaaatttcc acattttaig atcgtcaggt gacacgtacc 900
 gccaataact cggattattg tgtaaagtgg tataacactg gcttagataa attaaaaggt 960

acgaatgcig caagttggct gaagiatcac caatlcgaa gagaaatgac attacttggt 1020
 ttagatttag tagcgttatt tccaaactat gacacacgta cgtatccaat cgaaacaacg 1080
 gcccaactta cacgggaagt gtatcacagat ccaataglat ttaacagaga aacaagtgtt 1140
 ggattttgta ggcgltggic acttaacagt gataatttct tttcagaagt cgaaagcgct 1200
 glaattcggt caccacacct atttgatata ctacgtgaaa tagaatttta tacaacaaga 1260
 gcggggcttc ccttgaataa tacggaatlc ctitgaatatt gggtaggaca ttctataaaa 1320
 tataaaaaata cgaatgccic atcagcatla gaacgtlaatt acggtacgat tacttttaac 1380
 aaaaatcaagt attatgattt agcaataaag gatattcttc aggttcgac attaggggcg 1440
 gatttagcta attactacgc acaggtatat ggagttccgt acgctagttt tacactgctt 1500
 gacaagaata caggatcagg atcagttgga ggttttacgt actcaaaacc acatacaact 1560
 atgcaagtat gtacacaaaa ttacaatlcg attgatgaaa tccctccaga gaatgagcca 1620
 cttagtagag ggtatagcca tagattatct catatcacct ctatttcttt ttctaagaat 1680
 gctagtagic ctgctagata tggcaatcic cctgtatttg ctitggacaca tcggagtgcg 1740
 gattttacaa atacagtta ttacagataa attactcaga taccagtgtt aaaggcacat 1800
 actttagttt caggtactac tgttatlaaa ggtcctggat ttacaggagg caatatcctt 1860
 aaaaagaaca gtagtggctc gttagcttat actagtgtct ctgtaaaaic accattatca 1920
 caaagatata gtgcaagaat acgttatgct tctactacta acttacgact ttttgtaaca 1980
 atttctggaa ctgcattta ctctataaat gttataaaaa ccatgaataa aggggatgat 2040
 ttaacattta atacatttga cttagcaact attggtactg ctttcacatt ttcaaattac 2100
 tcggatagct taacggtagg tgcagattct ttgtcttcag gaggagaagt ttatgtagat 2160
 aagttcgaac ttattccggt aaatgcaaca ttigaagcag aagaagacct agatgtggca 2220
 aagaaagcag taaatggctt gtttacgagt aaaaaagatg ccttacagac aagtgtaacg 2280
 gattatcaag tgaatcaagc ggcaaaccta gtagaatgcc tatccgatga gttatacca 2340
 aatgaaaaac gaatgttatg ggatgcagtg aaagaggcga aacgactgtt tcaggcacgt 2400
 aacttactcc aagatacagg ctttaatagg attaatggag aaaacggatg gacgggaagt 2460
 acgggaatcg aggttcgga aggagatgtt ctgtttaaag atcgttcgct tcgtttgaca 2520
 agtgcgagag agattgatc agaaacatat ccaacgtatc tctatcaaca aatagatgaa 2580
 tcacttttaa aaccatatac aagatataaa ctaaaagggt ttataggaag tagtcaagat 2640
 ttagagattt aattaatcgc tcatcgggca aatcaaatcg tcaaaaatgt accagataat 2700
 ctcttgccag atgtactccc tgtcaattct tgtgttgga tcgatcgtc cagttagcaa 2760
 cagtatgtag acgcgaattt agcactcgaa aacaatggag aaaaatggaaa tatgtcttct 2820
 gattcccatg cattttcttt ccatattgat acaggtgaaa tagatttgaa tgaaaataca 2880
 ggaatttggg tcgtatttaa aattccgaca acaaatggat acgcaacact aggaaatctt 2940
 gaattggtag aagaggggccc attgtcaggg gaaacattag aacgagcaca acaacaagaa 3000
 caacaatggc aagacaaaaa ggcaagaaaa cgtggggcat cagaaaaagc atattatgca 3060
 gcaaagcaag ccatgatcgt tttaattcgca gattatcaag accaaaaact taattctggt 3120
 gtgaaatgt cagatatgtt ggcagcccaa aacctgtac agtccattcc ttacgtatat 3180
 aatgatgcgt taccagaaat ccttggatg aactatcga gttttacaga gttacaaat 3240

agacccaac aagcatggaa ttgtaigat ctacgaaatg ctataccaaa tggagatttt 3300
cgaaatggat taagtattg gaatgcaaca tcagatgtga atgtgcaaca actaagcgat 3360
acaatgtcc ttgtattcc aaactggaat tcacaaggt cacaacaatt tacagttaa 3420
ccgaattata gatattgttt acgtgtcaca gcgagaaaag agggagtagg agacggatat 3480
gtgatcatcc gtgatgggc gaatcagaca gaaacacica caattaatat atgtatgat 3540
gatacaggtg tttatctgc tgatcaaact agctatatca caaaaacagt ggaattcact 3600
ccaatcagag agcaagtgtg gatgacatg agtgagaccg aagggtatt caacatagaa 3660
agttagaac tcgtttaga agaagagtaa 3690